

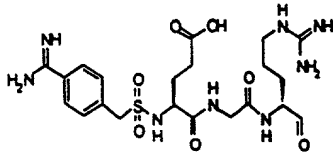
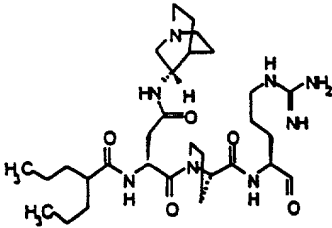
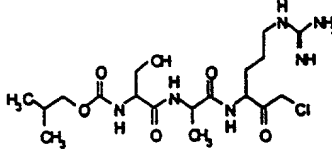
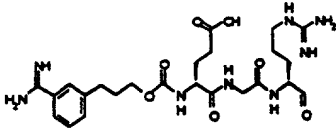
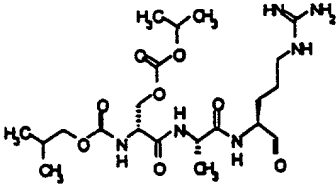
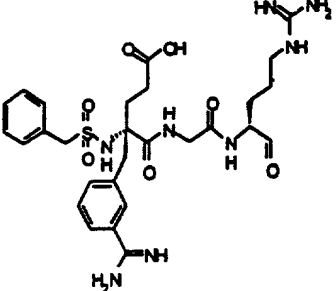
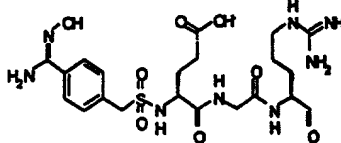
Compd #	MOLSTRUCTURE
1	
2	
3	
4	
5	
6	
7	

FIGURE 1A

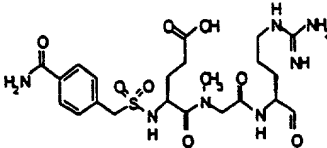
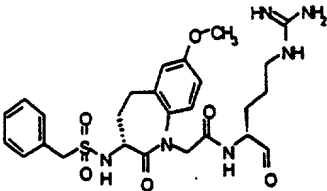
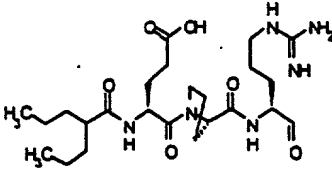
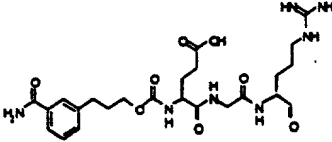
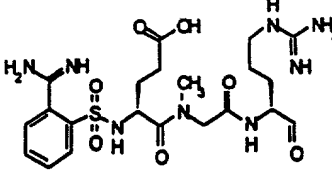
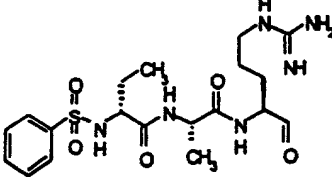
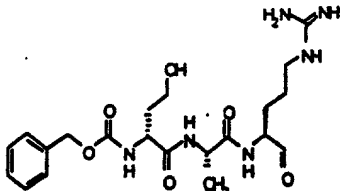
Compd #	MOLSTRUCTURE
8	
9	
10	
11	
12	
13	
14	

FIGURE 1B

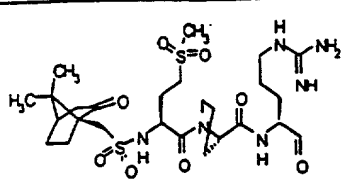
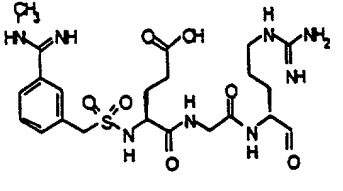
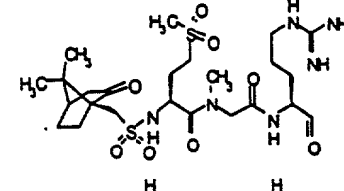
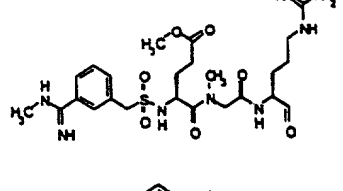
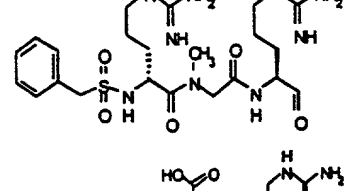
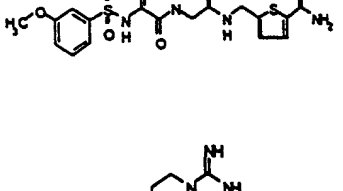
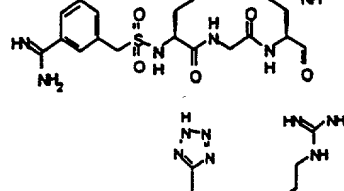
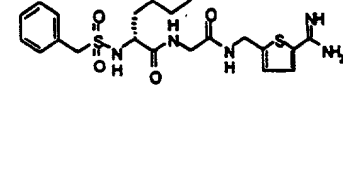
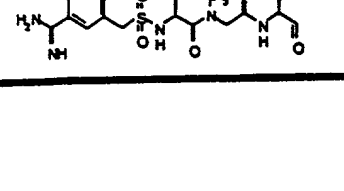
Compd #	MOLSTRUCTURE	Compd #	MOLSTRUCTURE
15		20	
16		21	
17		22	
18		23	
19			

FIGURE 1C

FIGURE 2A

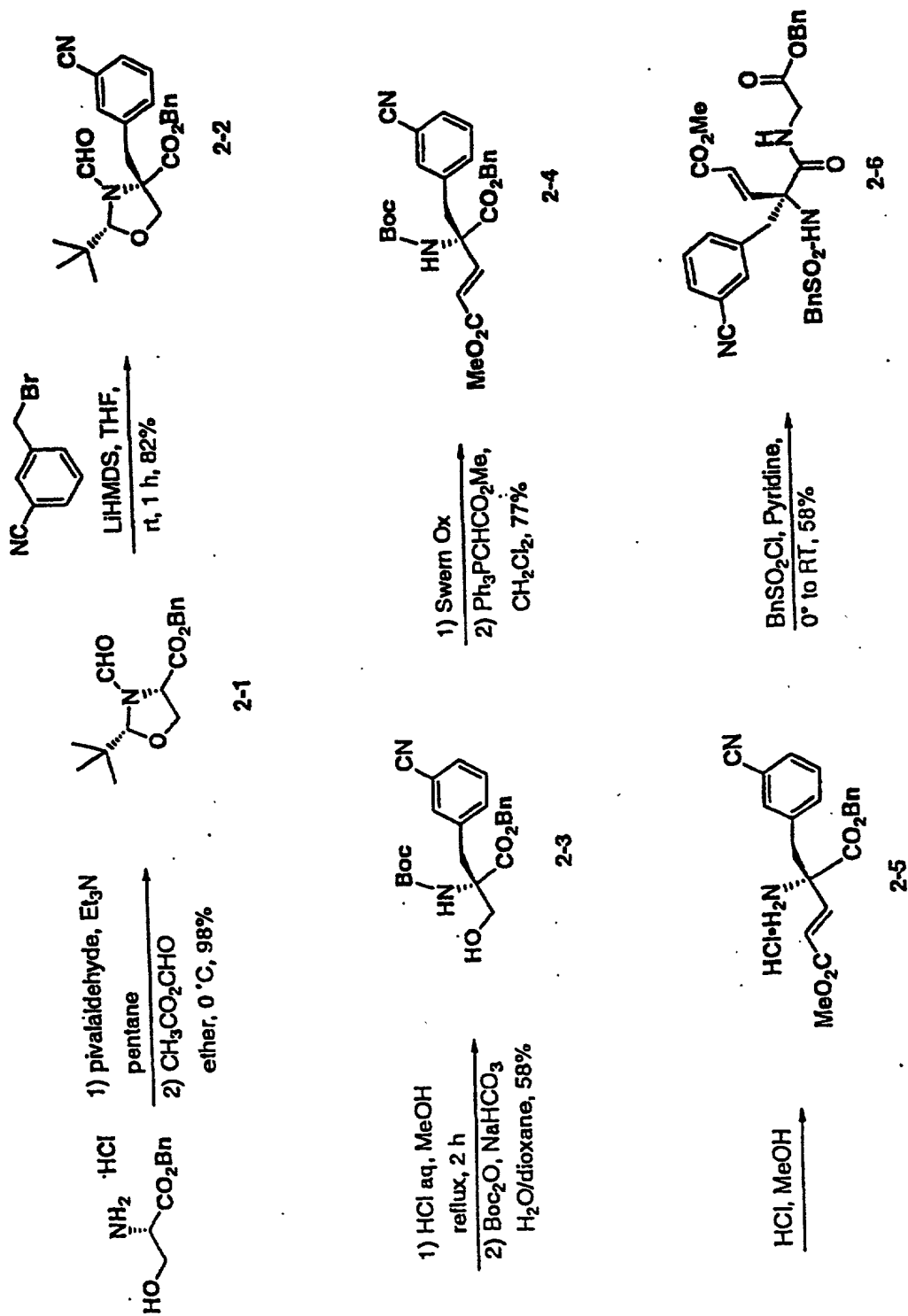
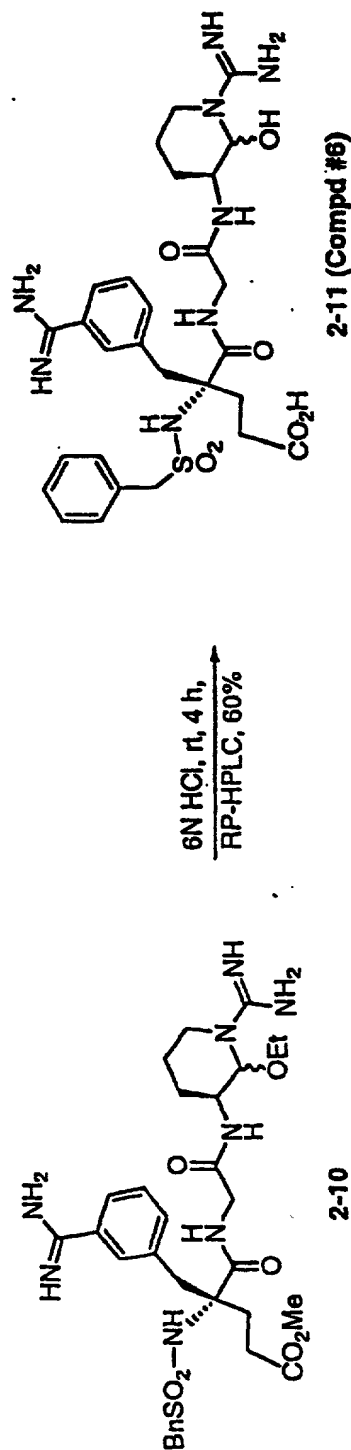
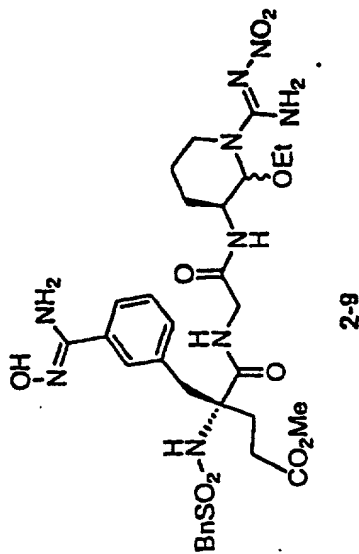
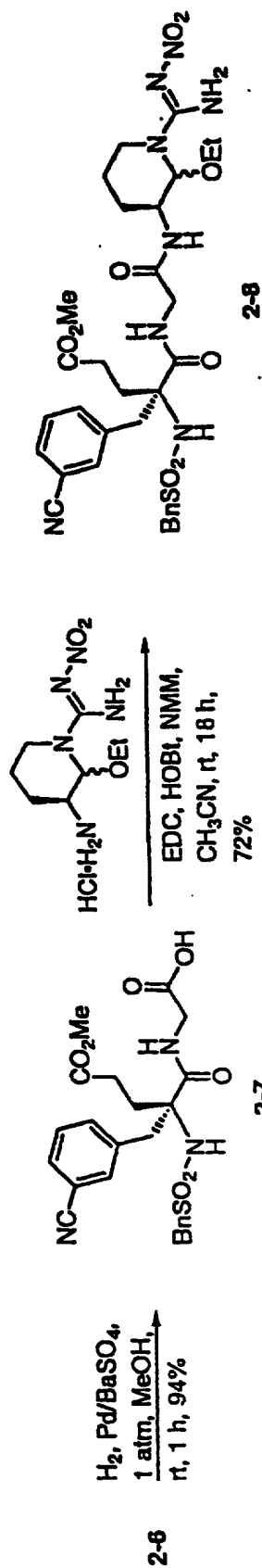


FIGURE 2B



2-11 (Compd #6)

10 20 30 40 50 60
 GTTGTGGGGGCACGGATGCGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCT
 CAACAACCCCGTGCCTACGCCTACTCCCCTCACCGGGACCGTCCATTTCGGACGTACGA
 V V G G T D A D E G E W P W Q V S L H A>
 70 80 90 100 110 120
 CTGGGCCAGGGCCACATCTGCGGTGCTTCCCTCATCTCTCCCAACTGGCTGGTCTCTGCC
 GACCCGGTCCCGGTGTAGACGCCACGAAGGGAGTAGAGAGGGTTGACCGACCAGAGACGG
 L G Q G H I C G A S L I S P N W L V S A>
 130 140 150 160 170 180
 GCACACTGCTACATCGATGACAGAGGATTCAGGTACTCAGACCCACGCAGTGGACGGCC
 CGTGTGACGATGTAGCTACTGTCTCCTAAGTCCATGAGTCTGGGGTGCCTCACCTGCCGG
 A H C Y I D D R G F R Y S D P T Q W T A>
 190 200 210 220 230 240
 TTCCTGGGCTTGACGACCAGAGCCAGCGCAGCGCCCTGGGGTGCAGGAGCGCAGGCTC
 AAGGACCCGAACGTGCTGGTCTCGGTGCGGTGCGGGGACCCACGTCTCTCGCGTCCGAG
 F L G L H D Q S Q R S A P G V Q E R R L>
 250 260 270 280 290 300
 AAGCGCATCATCTCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTG
 TTCGCGTAGTAGAGGGTGGGAAGAAGTTACTGAAGTGGAAGCTGATACTGTAGCGCGAC
 K R I I S H P F F N D F T F D Y D I A L>
 310 320 330 340 350 360
 CTGGAGCTGGAGAAACCGGCAGAGTACAGCTCCATGGTGGGCCCCTGCTGCCTGCCGGAC
 GACCTCGACCTCTTTGGCCGTCTCATGTCGAGGTACCACGCCGGGTAGACGGACGGCCTG
 L E L E K P A E Y S S M V R P I C L P D>

FIGURE 3A

370 380 390 400 410 420
 GCCTCCCATGTCTTCCCTGCCGGCAAGGCCATCTGGGTACGGGCTGGGGACACACCCAG
 CGGAGGGTACAGAAGGGACGGCCGTTCCGGTAGACCCAGTGCCCGACCCCTGTGTGGGTC
 A S H V F P A G K A I W V T G W G H T Q>

430 440 450 460 470 480
 TATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCATCAACCAGACC
 ATACCTCCGTGACCGCGCGACTAGGACGTTTTCCCACTCTAGGCGCAGTAGTTGGTCTGG
 Y G G T G A L I L Q K G E I R V I N Q T>

490 500 510 520 530 540
 ACCTGCGAGAACCTCCTGCCGCGCAGATCACGCCGCGCATGATGTGCGTGGGCTTCCTC
 TGGACGCTCTTGGAGGACGGCGCTCGTCTAGTGCGGCGCGTACTACACGCACCCGAAGGAG
 T C E N L L P Q Q I T P R M M C V G F L>

550 560 570 580 590 600
 AGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTGGAGGCG
 TCGCCGCGGCACCTGAGGACGGTCCCACTAAGGCCCCCTGGGGACAGGTCCGACCTCCGC
 S G G V D S C Q G D S G G P L S S V E A>

610 620 630 640 650 660
 GATGGGCGGATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGCTGCGCTCAGAGGAAC
 CTACCCGCCTAGAAGGTCCGGCCACACCACTCGACCCCTCTGCCGACGCGAGTCTCCTTG
 D G R I F Q A G V V S W G D G C A Q R N>

670 680 690 700 710 720
 AAGCCAGGCGGTACACAAGGCTCCCTCTGTTTCGGGACTGGATCAAAGAGAACACTGGG
 TTCGGTCCGCACATGTGTTCCGAGGGAGACAAAGCCCTGACCTAGTTTCTCTTGTGACCC
 K P G V Y T R L P L F R D W I K E N T G>

FIGURE 3B

GTATAG

CATATC

V *>

FIGURE 3C

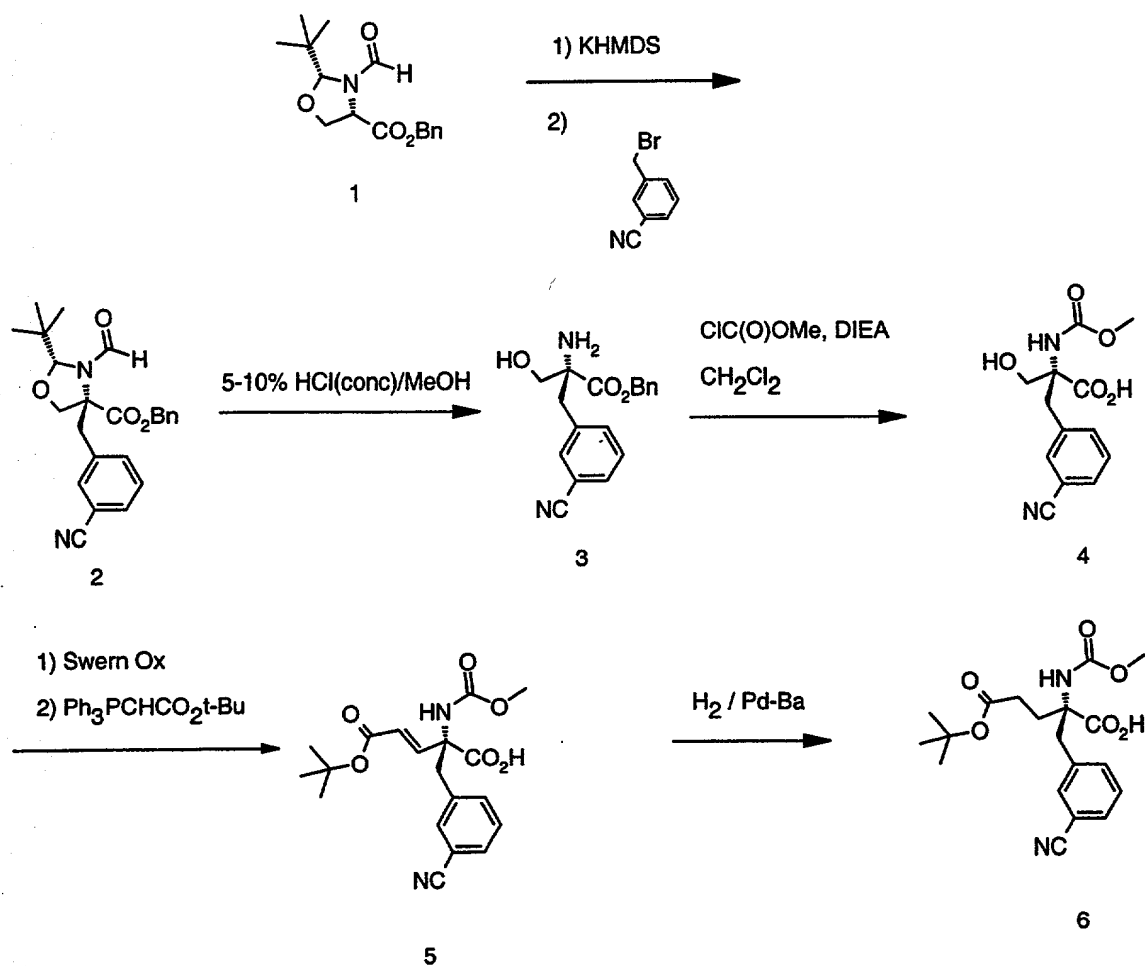


FIGURE 4A



FIGURE 4B

Compound	Structure
A	
B	
C	
D	
E	
F	
G	

FIGURE 5A

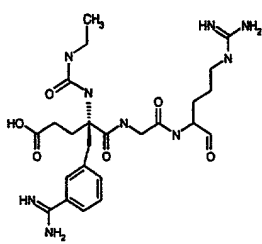
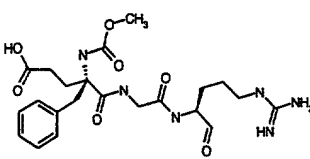
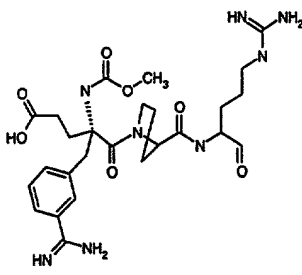
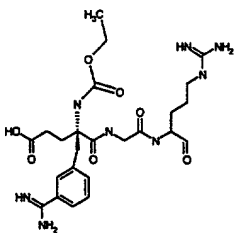
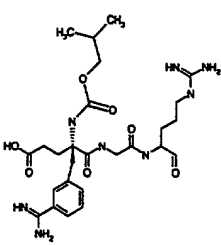
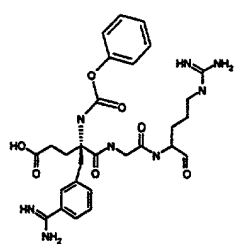
Compound	Structure
H	
I	
J	
K	
L	
M	

FIGURE 5B